This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

```
 1   <110> APPLICANT: Strachan, Lorna
 2         Sleeman, Matthew
 3         Abernethy, Nevin
 4         Onrust, Rene
 5         Kumble, Anand
 6         Murison, Greg
 7   <120> TITLE OF INVENTION: Compounds isolated from stromal cells
 8         and methods for their use
 9   <130> FILE REFERENCE: 11000.1037
10   <140> CURRENT APPLICATION NUMBER: US/09/276,268
11   <141> CURRENT FILING DATE: 1999-03-25
12   <160> NUMBER OF SEQ ID NOS: 20
13   <170> SOFTWARE: FastSEQ for Windows Version 3.0
14   <210> SEQ ID NO 1
15   <211> LENGTH: 803
16   <212> TYPE: DNA
17   <213> ORGANISM: Mouse
18   <400> SEQUENCE: 1
19         gttctgaatg ggagcatcag ccctctctgg gctgttgccc cgacattaca ggtcctgtct    60
20         ctcagggacg tgggccttgg ttctggcgct gcagagatgg acttctctgc gtttgggaat   120
21         ctgcgggcgt tggatctgtc gggaaactcc ctgaccagct tccaaaagtt caagggcagt   180
22         ttggcccttc ggactctcga cctccgcaga aactctctca cggccctccc tcagagggtt   240
23         gtgtccgagc agcctctgag gggtctgcag accatctacc tcagccagaa cccttatgac   300
24         tgctgtgggg tggaaggatg ggggggccctg cagcagcact tcaagactgt tgcggacttg   360
25         tccatggtca cttgcaacct ctcttccaag atcgtccgtg tggtggagct gcccgaaggc   420
26         ctgcctcagg gctgtaagtg ggaacaggtg gacactggtc tcttctacct cgtgctcatc   480
27         ctgcccagct gcctcaccct gctggtggcc tgtactgtcg tcttcctcac ttttaagaag   540
28         cctttgcttc aggtcatcaa gagccgctgc cactggtcct ccatatactg accgtgtgc    600
29         caaggctaga gacttggttt ttcctcgagg atgcgtctct ccgctggatc tttacttttg   660
30         caggggtcga gtgtgatgca ttgaaggtta aaactgaaat ttgaaagagt tccatcctca   720
31         gtcccattaa cttctcctcc catccgtgtg atttatcctc attgtcctgg tgaaatattt   780
32         attaaacgac attctgtgag att                                           803
33   <210> SEQ ID NO 2
34   <211> LENGTH: 689
35   <212> TYPE: DNA
36   <213> ORGANISM: Mouse
37   <220> FEATURE:
38   <221> NAME/KEY: CDS
39   <222> LOCATION: (35)...(556)
40   <400> SEQUENCE: 2
41         gtcgcctgag gtccccgccg acgacgcact cacc atg gcg cct gct aac ctt ggg    55
42                                                Met Ala Pro Ala Asn Leu Gly
43                                                 1                   5
44         ctg acg ccg cac tgg gtg atg ctc ctc ggt gcc gtg ctg ctg ttg ctt    103
```

```
45          Leu Thr Pro His Trp Val Met Leu Leu Gly Ala Val Leu Leu Leu Leu
46                     10              15                  20
47          ctg tcc gga gcc tcc gcg cag gaa cct ccg aga gtg ggt tgc tct gag    151
48          Leu Ser Gly Ala Ser Ala Gln Glu Pro Pro Arg Val Gly Cys Ser Glu
49                  25                  30                  35
50          tac aca aac aga tcc tgt gaa gag tgc ctc agg aat gtc tcc tgt ctg    199
51          Tyr Thr Asn Arg Ser Cys Glu Glu Cys Leu Arg Asn Val Ser Cys Leu
52           40                  45                  50                  55
53          tgg tgc aat gag aac aag gcg tgt atg gac tac cca gtg agg aaa atc    247
54          Trp Cys Asn Glu Asn Lys Ala Cys Met Asp Tyr Pro Val Arg Lys Ile
55                          60                  65                  70
56          ttg ccc cct gct tct ctc tgt aaa ttg agt tcc gct cgc tgg ggc gta    295
57          Leu Pro Pro Ala Ser Leu Cys Lys Leu Ser Ser Ala Arg Trp Gly Val
58                          75                  80                  85
59          tgc tgg gtg aac ttc gag gcc ttg atc atc acc atg tcg gtc ctg ggg    343
60          Cys Trp Val Asn Phe Glu Ala Leu Ile Ile Thr Met Ser Val Leu Gly
61                      90                  95                  100
62          ggc tct gtg ctc ctg ggc atc act gtg tgc tgc tgc tac tgc tgc cgc    391
63          Gly Ser Val Leu Leu Gly Ile Thr Val Cys Cys Cys Tyr Cys Cys Arg
64                  105                 110                 115
65          cgg aag aag agc cgg aag cca gac aag agc gat gag cgg gcc atg aga    439
66          Arg Lys Lys Ser Arg Lys Pro Asp Lys Ser Asp Glu Arg Ala Met Arg
67          120                 125                 130                 135
68          gag cag gag gag agg aga gtg cgg cag gag gaa agg agg gcg gaa atg    487
69          Glu Gln Glu Glu Arg Arg Val Arg Gln Glu Glu Arg Arg Ala Glu Met
70                          140                 145                 150
71          aag tca aga cat gat gaa atc agg aaa aaa tac ggt ctg ttt aaa gaa    535
72          Lys Ser Arg His Asp Glu Ile Arg Lys Lys Tyr Gly Leu Phe Lys Glu
73                          155                 160                 165
74          caa aac ccg tat gag aag ttc taaggtggct ggcacacact tgtggtggat    586
75          Gln Asn Pro Tyr Glu Lys Phe
76                      170
77          cgtgcagttc cagagtttcc tgggaatgca ctccccagca gagcctgcag agacctcacc   646
78          accatggcca cccttgacct gggtgatccc tcagcctcta ctg                    689
79    <210> SEQ ID NO 3
80    <211> LENGTH: 619
81    <212> TYPE: DNA
82    <213> ORGANISM: Mouse
83    <400> SEQUENCE: 3
84          ggcaccaggg aagccctgcc gcggcctgtc ccacagaacc tgcatcctca gatgccgccc     60
85          tatgcctttg ttcacccacc cttccccctg ccacctgtgc ggccgtgtt caacaacttc    120
86          cccatcaaca tgggtcctgt gcccgctccc tatgtccccc ctctgcccaa cgtgcgtgtc    180
87          aactatgact ttggccacat gcacgtgccc ctggagcaca acctgcccat gcactttggc    240
88          ccccaaccac ggcatcgctt ctgacaccca aagccctgtc agccgtgccg agtctgtagg    300
89          agggcccagt ctcatcttct gagtaggggt gaaggcctcc attccctctc gaaagtggac    360
90          gcgtgtcctc ctgctcttac ctttgcaagg tccatgctcc ttcaggtctg atgccctctg    420
91          ggtgctgatt gtcactgggc caattatagg gcagctccct agtctgccat cttagcagcc    480
92          aatccagtgg ccctgaccat gaagcaaggc ctctaatcgt ttgccatact tcctccccag    540
93          cagcccaatg aaagcccagg gggaaatggc ctaccatccc taagccaggg ctctctcctt    600
94          gttgcccaag gcccactta                                                619
```

```
 95   <210> SEQ ID NO 4
 96   <211> LENGTH: 1630
 97   <212> TYPE: DNA
 98   <213> ORGANISM: Mouse
 99   <220> FEATURE:
100   <221> NAME/KEY: CDS
101   <222> LOCATION: (46)...(849)
102   <221> NAME/KEY: sig_peptide
103   <222> LOCATION: (46)...(150)
104   <400> SEQUENCE: 4
105       ggcgcgtgag cctcaggatg aaccctgtgt ttcctagcgg gctgt atg gct ctc ggt    57
106                                                         Met Ala Leu Gly
107                                                         -35
108       ttt tct caa cgc tcc cgt atg gtg gcc gcg ggt gcc ggg gtg acc cgg   105
109       Phe Ser Gln Arg Ser Arg Met Val Ala Ala Gly Ala Gly Val Thr Arg
110           -30                 -25                 -20
111       ctg cta gtg ctc ttg ctg atg gta gcc gcg gct cct agc aga gcc cga   153
112       Leu Leu Val Leu Leu Leu Met Val Ala Ala Ala Pro Ser Arg Ala Arg
113       -15                 -10                 -5                  1
114       ggc agc ggc tgc cgg gtc ggg gcc tcc gcg cgt ggg acc ggg gcc gat   201
115       Gly Ser Gly Cys Arg Val Gly Ala Ser Ala Arg Gly Thr Gly Ala Asp
116                   5                   10                  15
117       ggc cgt gaa gct gag ggc tgt ggc acc gtg gct ttg ctg ctg gag cat   249
118       Gly Arg Glu Ala Glu Gly Cys Gly Thr Val Ala Leu Leu Leu Glu His
119                   20                  25                  30
120       tca ttt gag ctc ggt gat gga gcc aac ttc cag aag cga ggc ttg ctg   297
121       Ser Phe Glu Leu Gly Asp Gly Ala Asn Phe Gln Lys Arg Gly Leu Leu
122           35                  40                  45
123       ctc tgg aac cag cag gat ggc acc ctg tcg gca aca cag cga cag ctc   345
124       Leu Trp Asn Gln Gln Asp Gly Thr Leu Ser Ala Thr Gln Arg Gln Leu
125       50                  55                  60                  65
126       agt gag gag gag cgt ggc cga ctc cgg gat gtg gct gct gtc aat ggc   393
127       Ser Glu Glu Glu Arg Gly Arg Leu Arg Asp Val Ala Ala Val Asn Gly
128                   70                  75                  80
129       ctc tac agg gtc cgg gtc ccg agg cgg cct ggg aca ctt gat ggt tca   441
130       Leu Tyr Arg Val Arg Val Pro Arg Arg Pro Gly Thr Leu Asp Gly Ser
131                   85                  90                  95
132       gaa gct ggc ggc cat gtg tct tcc ttc gtc cca gcg tgc tcc ctg gtg   489
133       Glu Ala Gly Gly His Val Ser Ser Phe Val Pro Ala Cys Ser Leu Val
134                   100                 105                 110
135       gag tcg cac ctt tcg gac cag ctg acc ttg cac gtg gat gtg gct ggc   537
136       Glu Ser His Leu Ser Asp Gln Leu Thr Leu His Val Asp Val Ala Gly
137           115                 120                 125
138       aac gtg gtg ggc ctg tct gtg gtg gtg tac cct ggg ggc tgc cgg ggc   585
139       Asn Val Val Gly Leu Ser Val Val Val Tyr Pro Gly Gly Cys Arg Gly
140       130                 135                 140                 145
141       tcc gag gtg gaa gat gag gac ctg gag ctg ttc aat aca tct gtg cag   633
142       Ser Glu Val Glu Asp Glu Asp Leu Glu Leu Phe Asn Thr Ser Val Gln
143                   150                 155                 160
144       ctg cgg cct ccc agc act gct cca ggc ccc gag act gca gcc ttc att   681
```

```
145        Leu Arg Pro Pro Ser Thr Ala Pro Gly Pro Glu Thr Ala Ala Phe Ile
146                    165                 170                 175
147        gag cgc ctg gag atg gag cag gcc cag aag gcc aag aac cca cag gag    729
148        Glu Arg Leu Glu Met Glu Gln Ala Gln Lys Ala Lys Asn Pro Gln Glu
149                180                 185                 190
150        cag aag tct ttc ttt gcc aaa tac tgg atg tac atc att cca gtt gtg    777
151        Gln Lys Ser Phe Phe Ala Lys Tyr Trp Met Tyr Ile Ile Pro Val Val
152            195                 200                 205
153        ctg ttc ctc atg atg tcg gga gcg ccg gac gct ggg ggc cag ggc ggc    825
154        Leu Phe Leu Met Met Ser Gly Ala Pro Asp Ala Gly Gly Gln Gly Gly
155        210                 215                 220                 225
156        ggt ggg ggc ggg ggc agc agc cgg tgagcagctg tgccacctag agcccccccc   879
157        Gly Gly Gly Gly Gly Ser Ser Arg
158                        230
159        agagccagcc caagaaggag ttcctgaccc cacatttccc tattgcatga atatggaagg   939
160        ctgtcccttc agtgagccct ctggccttcc tgtaagcccc tctttctgtc cctgagcctc   999
161        tctctcatcc tgttgactga gagcttgggt ggacctccct gtagccagct cactgcaact  1059
162        gtgtcccacc atgtggcact gtgctcctct gtctgctaaa cacccaccag cctgccccac  1119
163        cccaccccac catacacttt gggaacttgc caagctctct ccagcctctg tgcctttgcc  1179
164        ctgcaggccc cgtgcgcccc tcactgtcac tctccagccc tttgccaagg atctgtggcc  1239
165        cagaggcctc tgctcttagt ggctaggtca gcctccagcc cactgtccag gtggcatgct  1299
166        gtcttctttg ccccctctc tggtgcccca gaataccatg gtgacctacc actatccttt   1359
167        ctgcctttgg atgtcatagc ctggatctgt caccaggaga ggattgtggg cctccacgtt  1419
168        agtctgtgaa tgcacacttc gagtgacttg tgtgcaggtt ttgagagccg gttttgcact  1479
169        agctgctcga cagctgctgg catggccgtg ctcttgcaca tgcgccgctg tgggcatggg  1539
170        gattgctgtg cagcctcagc tgtgttgtgt ggctgctgat taaactgtcc cctaaacagc  1599
171        aaaaaaaaaa aaaaaaaaaa aaaaaaaaa a                                 1630
172   <210> SEQ ID NO 5
173   <211> LENGTH: 1197
174   <212> TYPE: DNA
175   <213> ORGANISM: Mouse
176   <220> FEATURE:
177   <221> NAME/KEY: CDS
178   <222> LOCATION: (346)...(543)
179   <221> NAME/KEY: sig_peptide
180   <222> LOCATION: (346)...(420)
181   <400> SEQUENCE: 5
182        ggcaccagac gactggggcc ctaccccatg tggacaacct caccatgcgt ctggaccccg     60
183        gtgtgggcgc ctcagtgata ggcgtagtga cagtgacagt gacagctaga gggatgatag    120
184        acccccaaac tagtggactt tgaagttttc ttcccagccg gttccagcct cctggaacaa    180
185        ccatgtcgcc agttttgcgc gtgccaaatt cacggcgctg cccaagcgga gctgctatct    240
186        gaattctcct tggatgtggc aaagggaaat gaacgcaaaa ggtgccgctg aagtgtccg     300
187        acctagagaa atatgtagac cggagccctg ttccttcct ccagc atg gac ttc ctg     357
188                                                      Met Asp Phe Leu
189                                                      -25
190        gtt ctc ttc ttg ttc tac ttg gcc ttc tta ttg att tgt gtt gtc ctg     405
191        Val Leu Phe Leu Phe Tyr Leu Ala Phe Leu Leu Ile Cys Val Val Leu
192            -20                 -15                 -10
193        atc tgc atc ttc aca aaa agc cag cgt ttg aag gcc gtg gtc ctt gga     453
194        Ile Cys Ile Phe Thr Lys Ser Gln Arg Leu Lys Ala Val Val Leu Gly
```

```
195              -5                 1                 5                 10
196        gga gca cag gta gca ctg gtc ctt ggg tac tgc ccg gat gtg aat act      501
197        Gly Ala Gln Val Ala Leu Val Leu Gly Tyr Cys Pro Asp Val Asn Thr
198                    15                20                25
199        gtg tta ggt gct agt ctg gaa ggc tca caa gac aag ggg atg              543
200        Val Leu Gly Ala Ser Leu Glu Gly Ser Gln Asp Lys Gly Met
201                    30                35                40
202        tgagtcttgt ctttaatcct ggcacttggg aggctgaggc ttcggggcca gttggggcta    603
203        catcgcaaga gcctgtgtcc aaacaaacaa aacgttgtct ttttgctttg agataggtcg    663
204        aataggtcga attttcaagg ttggcttttt aaacagtgtg taatgtctgt atttggttgt    723
205        gactcctgtt tgcctagaca tgcttgtagc aggtgtgaac tcaggaggac acaagtgacc    783
206        agaaagctga gcatctagct gtcaatcttc ccttcacatt gtcccatctg tcttcccttg    843
207        ggggtcaaag caaagtgggg gcaagtagcc acgaaggggt tgacttggga ggaccctggg    903
208        gatctggagg ccaatcttga gcatggagca gacctgaggg ttagggaagc ccacgtccac    963
209        agcagcctct gcacacccc tttccccaca gactccaaca gacacattct gtgcagtcaa     1023
210        ggtagaaatg gaggtgttct ctacacctcc taaatcctag cacttaggaa gctgaggcag    1083
211        gattatgaat ccaggctag ctcgggttat gtaatgagac tgtttcaaac acagagcgga     1143
212        gccgaggaga tggctgggca gtcacagagc tgccgtgcaa ccagaactgg aggg           1197
213   <210> SEQ ID NO 6
214   <211> LENGTH: 1435
215   <212> TYPE: DNA
216   <213> ORGANISM: Mouse
217   <220> FEATURE:
218   <221> NAME/KEY: CDS
219   <222> LOCATION: (2)...(1015)
220   <221> NAME/KEY: sig_peptide
221   <222> LOCATION: (2)...(46)
222   <400> SEQUENCE: 6
223        c atg ggc gcc gtc tgg tca gcc ctg ctg gtc ggc ggg ggt cta gct gga      49
224          Met Gly Ala Val Trp Ser Ala Leu Leu Val Gly Gly Gly Leu Ala Gly
225         -15               -10               -5                1
226        gcg ctc atc ctg tgg ctg ctg cgg gga gac tct ggg gcc ccg ggg aaa       97
227        Ala Leu Ile Leu Trp Leu Leu Arg Gly Asp Ser Gly Ala Pro Gly Lys
228                     5                10                15
229        gac ggg gtt gcg gag ccg ccg cag aag ggc gca cct cct ggg gag gct      145
230        Asp Gly Val Ala Glu Pro Pro Gln Lys Gly Ala Pro Pro Gly Glu Ala
231                    20                25                30
232        gcg gcc ccg gga gac ggt ccg ggt ggt ggt ggc agt ggc ggc ctg agc     193
233        Ala Ala Pro Gly Asp Gly Pro Gly Gly Gly Gly Ser Gly Gly Leu Ser
234                    35                40                45
235        cct gaa cct tcc gat cgg gag ctg gtc tcc aaa gca gag cat ctt cga      241
236        Pro Glu Pro Ser Asp Arg Glu Leu Val Ser Lys Ala Glu His Leu Arg
237         50                55                60                65
238        gaa agc aac gga cat ttg att tct gag agc aaa gat ctt ggt aac ctg      289
239        Glu Ser Asn Gly His Leu Ile Ser Glu Ser Lys Asp Leu Gly Asn Leu
240                    70                75                80
241        ccg gaa gca cag cgg ctg cag aat gtt gga gca gac tgg gtc aat gcc      337
242        Pro Glu Ala Gln Arg Leu Gln Asn Val Gly Ala Asp Trp Val Asn Ala
243                    85                90                95
244        aga gag ttt gtt cct gtt ggg aag att cca gac aca cac tcc agg gcc      385
```

Input Set: **I276268.RAW**

| Line | ? | Error/Warning | Original Text |
|------|---|---------------|---------------|
| 288 | W | Invalid/Missing Amino Acid Numbering | |
| 291 | W | "N" or "Xaa" used: Feature required | cctgcagata atgcttcctg taanctggca cttgtccc |